Package 'VaSP'

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Type Package

Version 1.24.0

Title Quantification and Visualization of Variations of Splicing in Population

Description Discovery of genome-wide variable alternative splicing events from short-read RNA-seq data and visualizations of gene splicing information for publication-quality multi-panel figures in a population. (Warning: The visualizing function is removed due to the dependent package Sushi deprecated. If you want to use it, please change back to an older version.)

URL https://github.com/yuhuihui2011/VaSP

BugReports https://github.com/yuhuihui2011/VaSP/issues

License GPL (>= 2.0)

Depends R (>= 4.0), ballgown

Imports IRanges, GenomicRanges, S4Vectors, parallel, matrixStats, GenomicAlignments, GenomeInfoDb, Rsamtools, cluster, stats, graphics, methods

Suggests knitr, rmarkdown

VignetteBuilder knitr

biocViews RNASeq, AlternativeSplicing, DifferentialSplicing, StatisticalMethod, Visualization, Preprocessing, Clustering, DifferentialExpression, KEGG, ImmunoOncology

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`BMfinder` *Discover bimodal distrubition features*

Description

Find bimodal distrubition features and divide the samples into 2 groups by k-means clustering.

Usage

```
BMfinder(x, p.value = 0.01, maf = 0.05, miss = 0.05, fold = 2, log = FALSE,
        cores = detectCores() - 1)
```

Arguments

`x`	a numeric matrix with feature rows and sample columns, e.g., splicing score matrix from `spliceGenome` or `spliceGene` function.
`p.value`	p.value threshold for bimodal distrubition test
`maf`	minor allele frequency threshold in k-means clustering
`miss`	missing grouping rate threshold in k-means clustering
`fold`	fold change threshold between the two groups
`log`	whether the scores are to be logarithmic. If TRUE, all the scores are log2 tranformed before k-means clustering: x = log2(x+1).
`cores`	threads to be used. This value is passed to **?mclapply** in **parallel** package

Details

The matrix contains 1, 2 and NA, and values of 'x' in group 2 are larger than group 1.

Value

a matrix with feature rows and sample columns.

Examples

```
data(rice.bg)
score<-spliceGene(rice.bg,'MSTRG.183',junc.type='score')
score<-round(score,2)
as<-BMfinder(score,cores=1) # 4 bimodal distrubition features found

##compare
as
score[rownames(score)%in%rownames(as),]
```

`getDepth` *Get Read Depth*

Description

Get read depth from a BAM file (in bedgraph format)

Usage

```
getDepth(x, chrom, start, end)
```

Arguments

`x`	path to a BAM file
`chrom`	chromosome of a region to be searched
`start`	start position
`end`	end position

Value

a data.frame in bedgraph file format.

Examples

```
path <- system.file('extdata',package='VaSP')
bam_files<-list.files(path,'bam$')
bam_files

depth<-getDepth(file.path(path, bam_files[1]), 'Chr1',
                start=1171800, end=1179400)
head(depth)

# library(Sushi)
# plotBedgraph(depth,'Chr1',chromstart=1171800, chromend=1179400,yaxt='s')
```

```
# mtext('Depth',side=2,line=2.5,cex=1.2,font=2)
# labelgenome('Chr1',1171800,1179400,side=1,scipen=20,n=5,scale='Kb')
```

---

getGeneinfo *Get Gene Informaton from a ballgown object*

Description

Get gene informaton from a ballgown object by genes or by genomic regions

Usage

```
getGeneinfo(genes = NA, bg, chrom, start, end, samples = sampleNames(bg),
            trans.select = NA)
```

Arguments

genes	a character vector specifying gene IDs in 'bg'. Any values other than NA override genomic region (chrom, start, stop)
bg	ballgown object
chrom	chromosome of a region
start	start postion
end	stop postion
samples	names of samples. The transcrpts in these samples are subjected to 'trans.select'
trans.select	logical expression-like string, indicating transcript rows to select from a matrix of transcript coverages: NA value keeps all transcripts.

Value

a data.frame in bed-like file format

Examples

```
data(rice.bg)
unique(geneIDs(rice.bg))

gene_id <- c('MSTRG.181', 'MSTRG.182', 'MSTRG.183')
geneinfo <- getGeneinfo(genes=gene_id,rice.bg)
trans <- table(geneinfo$name) # show how many exons each transcript has
trans

# library(Sushi)
# chrom = geneinfo$chrom[1]
# chromstart = min(geneinfo$start) - 1e3
# chromend = max(geneinfo$stop) + 1e3
# color = rep(SushiColors(2)(length(trans)), trans)
```

```
# par(mar=c(3,1,1,1))
# plotGenes(geneinfo, chrom, chromstart, chromend, col = color, bheight = 0.2,
#           bentline = FALSE, plotgenetype = 'arrow', labeloffset = 0.5)
# labelgenome(chrom, chromstart , chromend, side = 1, n = 5, scale = 'Kb')
```

`rice.bg` *Rice ballgown object*

Description

Small ballgown object created with a subset of rice RNAseq data, for demonstration purposes

Format

a ballgown object with 33 transcripts and 6 samples

Details

The raw RNA-seq data were screened and trimmed using Trimmomatic (Bolger et al., 2014) and RNA-seq mapping, transcript assembly, and quantification were conducted with HISAT, StringTie, and Ballgown by following the method described by Pertea et al. (Pertea et al., 2016). The rice.bg is a subset ballgown object with 33 transcripts and 6 samples (Yu et al., 2021).

Source

The raw RNA-seq data were from the project of variation in transcriptional responses to salt stress in rice (SRA Accession: SRP106054)

References

Yu, H., Du, Q., Campbell, M., Yu, B., Walia, H. and Zhang, C. (2021), Genome-wide discovery of natural variation in pre-mRNA splicing and prioritising causal alternative splicing to salt stress response in rice. New Phytol. https://doi.org/10.1111/nph.17189

Bolger, A.M., Lohse, M., and Usadel, B. (2014). Trimmomatic: a flexible trimmer for Illumina sequence data. Bioinformatics 30, 2114-2120.

Pertea, M., Kim, D., Pertea, G.M., Leek, J.T., and Salzberg, S.L. (2016). Transcript-level expression analysis of RNA-seq experiments with HISAT, StringTie and Ballgown. Nat Protoc 11, 1650-1667.

Examples

```
data(rice.bg)
rice.bg
# ballgown instance with 33 transcripts and 6 samples
```

spliceGene *Calculate Splicing Scores for One Gene*

Description

Calculate splicing Scores from ballgown object for a given gene. This function can only calculate one gene. Please use function spliceGenome to obtain genome-wide splicing scores.

Usage

```
spliceGene(bg, gene, samples = sampleNames(bg), junc.type = c("score", "count"),
           trans.select = "rowMaxs(x)>=1", junc.select = "rowMaxs(x)>=5")
```

Arguments

bg	ballgown object
gene	a character string specifying gene id
samples	names of samples
junc.type	type of junction estimate ('score' for junction score; 'count' for junction read count)
trans.select	logical expression-like string, indicating transcript rows to select from a matrix of transcript coverages: NA value keeps all transcripts. e.g. use trans.select='rowMaxs(x)>=1' to filter the transcrpts with the maximium coverage among all the samples less than 1.
junc.select	logical expression-like string, indicating junction rows to select from a matrix of junction counts: NA value keeps all junctions. e.g. use junc.select='rowMaxs(x)>=5' to filter the junctions with the maximium read count among all the samples less than 5.

Details

score = junction count/gene-level per base read coverage. Row functions for matrices are useful to select transcripts and junctions. See matrixStats package.

Value

a matrix of junction scores with intron rows and sample columns.

References

Yu, H., Du, Q., Campbell, M., Yu, B., Walia, H. and Zhang, C. (2021), Genome-wide discovery of natural variation in pre-mRNA splicing and prioritising causal alternative splicing to salt stress response in rice. New Phytol. https://doi.org/10.1111/nph.17189

See Also

spliceGenome, which calculates splicing scores in whole genome.

Examples

```
data(rice.bg)
rice.bg
head(geneIDs(rice.bg))

score<-spliceGene(rice.bg,'MSTRG.183',junc.type='score')
count<-spliceGene(rice.bg,'MSTRG.183',junc.type='count')

## compare
tail(score)
tail(count)

## get intron structrue
intron<-structure(rice.bg)$intron
intron[intron$id%in%rownames(score)]
```

`spliceGenome` *Calculate Genome-wide Splicing Scores*

Description

Calculate splicing scores from ballgown objects for all genes.

Usage

```
spliceGenome(bg, gene.select = "rowQuantiles(x,probs = 0.05)>=1",
            intron.select = "rowQuantiles(x,probs = 0.95)>=5")
```

Arguments

`bg`	ballgown object
`gene.select`	logical expression-like string, indicating genes to select from a matrix of gene-level coverages: NA value keeps all genes. e.g. gene.select = 'rowQuantiles(x,probs = 0.05)>=1' keeps the genes with the read coverage greater than or equal to 1 in at least 95 (0.05 quantile). Used to filter low expressed genes.
`intron.select`	logical expression-like string, indicating introns to select from a matrix of junction counts: NA value keeps all introns. e.g. intron.select = 'rowQuantiles(x,probs = 0.95)>=5' keeps the introns with the read count greater than or euqal to 5 in at least 5 (0.95 quantile). Used to filter introns with very few junction reads supporting.

Details

score = junction count/gene-level per base read coverage. Row functions for matrices in `matrixStats` package are useful to select genes and introns.

Value

a list of two elelments: 'score' is matrix of intron splicing scores with intron rows and sample columns and 'intron' is a GRanges object of intron structure. See structure in **ballgown** package

References

Yu, H., Du, Q., Campbell, M., Yu, B., Walia, H. and Zhang, C. (2021), Genome-wide discovery of natural variation in pre-mRNA splicing and prioritising causal alternative splicing to salt stress response in rice. New Phytol. https://doi.org/10.1111/nph.17189

See Also

spliceGene, which calculates splicing scores in one gene.

Examples

```
data(rice.bg)
rice.bg

splice<-spliceGenome(rice.bg,gene.select=NA,intron.select=NA)
names(splice)

head(splice$score)
splice$intron
```

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